



SEQUENCE LISTING

<110> CHIANG, VINCENT L.
CARRAWAY, DANIEL T.
SMELTZER, RICHARD H.

<120> PRODUCTION OF SYRINGYL LIGNIN IN GYMNOSPERMS

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<141> 2003-10-09

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Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys Val Ala Lys	
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Pro Leu Tyr
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Val	Arg	Val	Val	Ala	Ser	Asn	Ile	Gly	Ser	Thr	Val	Asn	Ile	Gly	Glu	165	170	175	
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Leu Ser Leu Met Asn Gln Asp Lys Val Leu Met Glu Ser Trp Tyr His
130 135 140
Leu Thr Glu Ala Val Leu Glu Gly Gly Ile Pro Phe Asn Lys Ala Tyr
145 150 155 160

Gly Met Thr Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Thr
 165 170 175
 Val Phe Asn Asn Gly Met Ser Asn His Ser Thr Ile Thr Met Lys Lys
 180 185 190
 Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu Gly Ser Val Val Asp
 195 200 205
 Val Gly Gly Gly Thr Gly Ala His Leu Asn Met Ile Ile Ala Lys Tyr
 210 215 220
 Pro Met Ile Lys Gly Ile Asn Phe Asp Leu Pro His Val Ile Glu Glu
 225 230 235 240
 Ala Pro Ser Tyr Pro Gly Val Glu His Val Gly Gly Asp Met Phe Val
 245 250 255
 Ser Val Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Cys His Asp
 260 265 270
 Trp Ser Asp Glu His Cys Leu Lys Phe Leu Lys Lys Cys Tyr Glu Ala
 275 280 285
 Leu Pro Thr Asn Gly Lys Val Ile Leu Ala Glu Cys Ile Leu Pro Val
 290 295 300
 Ala Pro Asp Ala Ser Leu Pro Thr Lys Ala Val Val His Ile Asp Val
 305 310 315 320
 Ile Met Leu Ala His Asn Pro Gly Gly Lys Glu Arg Thr Glu Lys Glu
 325 330 335
 Phe Glu Ala Leu Ala Lys Gly Ala Gly Phe Glu Gly Phe Arg Val Val
 340 345 350
 Ala Ser Cys Ala Tyr Asn Thr Trp Ile Ile Glu Phe Leu Lys Lys Ile
 355 360 365

<210> 7
 <211> 2025
 <212> DNA
 <213> Liquidambar styraciflua

<220>
 <221> CDS
 <222> (60)..(1679)

<400> 7
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atg gag acc caa aca aaa caa gaa gaa atc ata tat cgg tcg aaa ctc 107
 Met Glu Thr Gln Thr Lys Gln Glu Glu Ile Ile Tyr Arg Ser Lys Leu
 1 5 10 15

ccc gat atc tac atc ccc aaa cac ctc cct tta cat tcg tat tgt ttc	155
Pro Asp Ile Tyr Ile Pro Lys His Leu Pro Leu His Ser Tyr Cys Phe	
20 25 30	
gag aac atc tca cag ttc ggc tcc cgc ccc tgt ctg atc aat ggc gca	203
Glu Asn Ile Ser Gln Phe Gly Ser Arg Pro Cys Leu Ile Asn Gly Ala	
35 40 45	
acg ggc aag tat tac aca tat gct gag gtt gag ctc att gcg cgc aag	251
Thr Gly Lys Tyr Tyr Thr Tyr Ala Glu Val Glu Leu Ile Ala Arg Lys	
50 55 60	
gtc gca tcc ggc ctc aac aaa ctc ggc gtt cga caa ggt gac atc atc	299
Val Ala Ser Gly Leu Asn Lys Leu Gly Val Arg Gln Gly Asp Ile Ile	
65 70 75 80	
atg ctt ttg cta ccc aac tcg ccg gag ttc gtg ttt tca att ctc ggc	347
Met Leu Leu Leu Pro Asn Ser Pro Glu Phe Val Phe Ser Ile Leu Gly	
85 90 95	
gca tcc tac cgc ggg gct gcc gcc acc gcc gca aac ccg ttt tat acc	395
Ala Ser Tyr Arg Gly Ala Ala Ala Thr Ala Ala Asn Pro Phe Tyr Thr	
100 105 110	
cct gcc gag atc agg aag caa gcc aaa acc tcc aac gcc agg ctt att	443
Pro Ala Glu Ile Arg Lys Gln Ala Lys Thr Ser Asn Ala Arg Leu Ile	
115 120 125	
atc aca cat gcc tgt tac tat gag aaa gtg aag gac ttg gtg gaa gag	491
Ile Thr His Ala Cys Tyr Tyr Glu Lys Val Lys Asp Leu Val Glu Glu	
130 135 140	
aac gtt gcc aag atc ata tgt ata gac tca ccc ccg gac ggt tgt ttg	539
Asn Val Ala Lys Ile Ile Cys Ile Asp Ser Pro Pro Asp Gly Cys Leu	
145 150 155 160	
cac ttc tcg gag ctg agt gag gcg gac gag aac gac atg ccc aat gta	587
His Phe Ser Glu Leu Ser Glu Ala Asp Glu Asn Asp Met Pro Asn Val	
165 170 175	
gag att gac ccc gat gat gtg gtg gcg ctg ccg tac tcg tca ggg acg	635
Glu Ile Asp Pro Asp Asp Val Val Ala Leu Pro Tyr Ser Ser Gly Thr	
180 185 190	
acg ggt tta cca aag ggg gtg atg cta aca cac aag gga caa gtg acg	683
Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Gly Gln Val Thr	
195 200 205	
agt gtg gcg caa cag gtg gac gga gag aat ccg aac ctg tat ata cat	731
Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro Asn Leu Tyr Ile His	
210 215 220	
agc gag gac gtg gtt ctg tgc gtg ttg cct ctg ttt cac atc tac tcg	779
Ser Glu Asp Val Val Leu Cys Val Leu Pro Leu Phe His Ile Tyr Ser	
225 230 235 240	

atg aac gtc atg ttt tgc ggg tta cga gtt ggt gcg gcg att ctg att	827
Met Asn Val Met Phe Cys Gly Leu Arg Val Gly Ala Ala Ile Leu Ile	
245 250 255	
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Met Gln Lys Phe Glu Ile Tyr Gly Leu Leu Glu Leu Val Arg Ser Thr	
260 265 270	
ggt gac cat cat gcc tat cgt aca ccc atc gta ttg gca atc tcc aag	923
Gly Asp His His Ala Tyr Arg Thr Pro Ile Val Leu Ala Ile Ser Lys	
275 280 285	
act ccg gat ctt cac aac tat gat gtg tcc tcc att cgg act gtc atg	971
Thr Pro Asp Leu His Asn Tyr Asp Val Ser Ser Ile Arg Thr Val Met	
290 295 300	
tca ggt gcg gct cct ctg ggc aag gaa ctt gaa gat tct gtc aga gct	1019
Ser Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Ser Val Arg Ala	
305 310 315 320	
aag ttt ccc acc gcc aaa ctt ggt cag gga tat gga atg acg gag gca	1067
Lys Phe Pro Thr Ala Lys Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala	
325 330 335	
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Gly Pro Val Leu Ala Met Cys Leu Ala Phe Ala Lys Glu Gly Phe Glu	
340 345 350	
ata aaa tcg ggg gca tct gga act gtt tta agg aac gca cag atg aag	1163
Ile Lys Ser Gly Ala Ser Gly Thr Val Leu Arg Asn Ala Gln Met Lys	
355 360 365	
att gtg gac cct gaa acc ggt gtc act ctc cct cga aac caa ccc gga	1211
Ile Val Asp Pro Glu Thr Gly Val Thr Leu Pro Arg Asn Gln Pro Gly	
370 375 380	
gag att tgc att aga gga gac caa atc atg aaa ggt tat ctt aat gat	1259
Glu Ile Cys Ile Arg Gly Asp Gln Ile Met Lys Gly Tyr Leu Asn Asp	
385 390 395 400	
cct gag gcg acg gag aga acc ata gac aag gaa ggt tgg tta cac aca	1307
Pro Glu Ala Thr Glu Arg Thr Ile Asp Lys Glu Gly Trp Leu His Thr	
405 410 415	
ggt gat gtg ggc tac atc gac gat gac act gag ctc ttc att gtt gat	1355
Gly Asp Val Gly Tyr Ile Asp Asp Thr Glu Leu Phe Ile Val Asp	
420 425 430	
cgg ttg aag gaa ctg atc aaa tac aaa ggg ttt cag gtg gca ccc gct	1403
Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala	
435 440 445	
gag ctt gag gcc atg ctc ctc aac cat ccc aac atc tct gat gct gcc	1451
Glu Leu Glu Ala Met Leu Leu Asn His Pro Asn Ile Ser Asp Ala Ala	
450 455 460	

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gtc gtc cca atg aaa gac gat gaa gct gga gag ctc cct gtg gcg ttt 1499
Val Val Pro Met Lys Asp Asp Glu Ala Gly Glu Leu Pro Val Ala Phe
465                      470                      475                      480

gtt gta aga tca gat ggt tct cag ata tcc gag gct gaa atc agg caa 1547
Val Val Arg Ser Asp Gly Ser Gln Ile Ser Glu Ala Glu Ile Arg Gln
                      485                      490                      495

tac atc gca aaa cag gtg gtt ttt tat aaa aga ata cat cgc gta ttt 1595
Tyr Ile Ala Lys Gln Val Val Phe Tyr Lys Arg Ile His Arg Val Phe
                      500                      505                      510

ttc gtc gaa gcc att cct aaa gcg ccc tct ggc aaa atc ttg cgg aag 1643
Phe Val Glu Ala Ile Pro Lys Ala Pro Ser Gly Lys Ile Leu Arg Lys
                      515                      520                      525

gac ctg aga gcc aaa ttg gcg tct ggt ctt ccc aat taattctcat 1689
Asp Leu Arg Ala Lys Leu Ala Ser Gly Leu Pro Asn
                      530                      535                      540

tcgctaccct cctttctctt atcatcgcgc aacacgaacg aagaggctca attaaacgct 1749

gctcattcga agcggctcaa ttaaagctgc tcattcatgt ccaccgagtg ggcagcctgt 1809

cttggtggga tgttctttca tttgattcag ctgtgagaag ccagaccctc attatatttatt 1869

gtgaaattca caagaatgtc tgtaaatacga tggtgtgagt gatgggtttc aaaacacttt 1929

tgacattgtt tacgttgtat ttctgtctgt tgaaaataac tactttgtat gactttttatt 1989

tggaagata acctttcaaa aaaaaaaaaa aaaaaa 2025

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<210> 8
<211> 540
<212> PRT
<213> Liquidambar styraciflua

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<400> 8
Met Glu Thr Gln Thr Lys Gln Glu Glu Ile Ile Tyr Arg Ser Lys Leu
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Pro Asp Ile Tyr Ile Pro Lys His Leu Pro Leu His Ser Tyr Cys Phe
                20                      25                      30

Glu Asn Ile Ser Gln Phe Gly Ser Arg Pro Cys Leu Ile Asn Gly Ala
    35                      40                      45

Thr Gly Lys Tyr Tyr Thr Tyr Ala Glu Val Glu Leu Ile Ala Arg Lys
    50                      55                      60

Val Ala Ser Gly Leu Asn Lys Leu Gly Val Arg Gln Gly Asp Ile Ile
    65                      70                      75                      80

Met Leu Leu Leu Pro Asn Ser Pro Glu Phe Val Phe Ser Ile Leu Gly
                85                      90                      95

```


Ala	Ser	Tyr	Arg	Gly	Ala	Ala	Ala	Thr	Ala	Ala	Asn	Pro	Phe	Tyr	Thr	100	105	110	
Pro	Ala	Glu	Ile	Arg	Lys	Gln	Ala	Lys	Thr	Ser	Asn	Ala	Arg	Leu	Ile	115	120	125	
Ile	Thr	His	Ala	Cys	Tyr	Tyr	Glu	Lys	Val	Lys	Asp	Leu	Val	Glu	Glu	130	135	140	
Asn	Val	Ala	Lys	Ile	Ile	Cys	Ile	Asp	Ser	Pro	Pro	Asp	Gly	Cys	Leu	145	150	155	160
His	Phe	Ser	Glu	Leu	Ser	Glu	Ala	Asp	Glu	Asn	Asp	Met	Pro	Asn	Val	165	170	175	
Glu	Ile	Asp	Pro	Asp	Asp	Val	Val	Ala	Leu	Pro	Tyr	Ser	Ser	Gly	Thr	180	185	190	
Thr	Gly	Leu	Pro	Lys	Gly	Val	Met	Leu	Thr	His	Lys	Gly	Gln	Val	Thr	195	200	205	
Ser	Val	Ala	Gln	Gln	Val	Asp	Gly	Glu	Asn	Pro	Asn	Leu	Tyr	Ile	His	210	215	220	
Ser	Glu	Asp	Val	Val	Leu	Cys	Val	Leu	Pro	Leu	Phe	His	Ile	Tyr	Ser	225	230	235	240
Met	Asn	Val	Met	Phe	Cys	Gly	Leu	Arg	Val	Gly	Ala	Ala	Ile	Leu	Ile	245	250	255	
Met	Gln	Lys	Phe	Glu	Ile	Tyr	Gly	Leu	Leu	Glu	Leu	Val	Arg	Ser	Thr	260	265	270	
Gly	Asp	His	His	Ala	Tyr	Arg	Thr	Pro	Ile	Val	Leu	Ala	Ile	Ser	Lys	275	280	285	
Thr	Pro	Asp	Leu	His	Asn	Tyr	Asp	Val	Ser	Ser	Ile	Arg	Thr	Val	Met	290	295	300	
Ser	Gly	Ala	Ala	Pro	Leu	Gly	Lys	Glu	Leu	Glu	Asp	Ser	Val	Arg	Ala	305	310	315	320
Lys	Phe	Pro	Thr	Ala	Lys	Leu	Gly	Gln	Gly	Tyr	Gly	Met	Thr	Glu	Ala	325	330	335	
Gly	Pro	Val	Leu	Ala	Met	Cys	Leu	Ala	Phe	Ala	Lys	Glu	Gly	Phe	Glu	340	345	350	
Ile	Lys	Ser	Gly	Ala	Ser	Gly	Thr	Val	Leu	Arg	Asn	Ala	Gln	Met	Lys	355	360	365	
Ile	Val	Asp	Pro	Glu	Thr	Gly	Val	Thr	Leu	Pro	Arg	Asn	Gln	Pro	Gly	370	375	380	
Glu	Ile	Cys	Ile	Arg	Gly	Asp	Gln	Ile	Met	Lys	Gly	Tyr	Leu	Asn	Asp	385	390	395	400

[illegible]

```

attcaagaat tcaattgccc tgccctgctc tgctctgctt tgctcaactt attgatccct 1440
gctctggttt gttcaatttc ttgacccttg ctgggttctg ctctggtttg cacactttct 1500
cgattatata agtcattttg gatccttgca aggaagagaa tatg 1544

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<210> 10
<211> 659
<212> DNA
<213> Pinus taeda

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<400> 10
aaacaccaat ttaatgggat ttcagatttg tatcccatgc tattgggctaa ggcatttttc 60
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ccgaaaacag cgaatgaaat gtctgggtga tcggtcaaac aagcgggtgg cgagagagcg 180
cgggtgttgg cctagccggg atgggggtag gtagacggcg tattaccggc gagttgtccg 240
aatggagttt tcggggtagg tagtaacgta gacgtcaatg gaaaaagtca taatctccgt 300
caaaaatcca accgctcctt cacatcgtag agttggtggc cacgggaccc tccaccact 360
cactcaatcg atcgctgcc gtggttgccc attattcaac catacgccac ttgactcttc 420
accaacaatt ccaggccggc tttctataca atgtactgca caggaaaatc caatataaaa 480
agccggcctc tgcttccttc tcagtagccc ccagctcatt caattcttcc cactgcaggc 540
tacatttgtc agacacgttt tccgccattt ttcgcctgtt tctgcggaga atttgatcag 600
gttcggattg ggattgaatc aattgaaagg tttttatttt cagtatttcg atcgccatg 659

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<210> 11
<211> 2251
<212> DNA
<213> Pinus taeda

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<400> 11
ggcggggttg tgacatttat tcataaatc atctcaaac aagaaggatt tacaaaaata 60
aaagaaaaca aaattttcat ctttaacata attataattg tgttcacaaa attcaactt 120
aaaccttaa tataaagaat ttctttcaac aatacacttt aatcacact tcttcaatca 180
caacctctc caacaaaatt aaaatagatt aataaataaa taaacttaac tatttaaaaa 240
aaaatattat acaaaattta ttaaaacttc aaaataaaca aactttttat acaaaattca 300
tcaaaacttt aaaataaagc taacactga aaatgtgagt acatttaaaa ggacgtgat 360
cacaaaatt ttgaaaacat aaacaaactt gaaactctac cttttaagaa tgagtttgtc 420
gtctcattaa ctcatagtt ttatagttcg aatccaatta acgtatcttt tattttatgg 480
aataaggggtg ttttaataag tgattttggg attttttttag taatttattt gtgatattgt 540
atggagtttt taaaaatata tatatatata tatatttttg ggttgagttt acttaaaatt 600
tggaaggggt tggtagaagc tataaattga gttgtgaatg agtgttttat ggatttttta 660
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aaattaattt taaatttaata aacttttgaa gtcaaatatt ccaaatattt tccaaaatat 900
taaactctatt ttgcattcaa aatacaattt aaataataaa acttcatgga atagattaac 960
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caaaatcatt acattaaagc tcatcatgtc atttgtggat tggaaattat attgtataag 1260
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tttattggaa tgaaggttga gttataaact ttcagtaatc caagtatctt cggtttttga 1560
agatactaaa tccattatat aataaaaaa cattttaaac accaatttaa tgggatttca 1620
gatttgtatc ccatgtctatt ggctaaggca tttttcttat tgtaatctaa ccaattctaa 1680

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tttccaccct ggtgtgaact gactgacaaa tgcggtccga aaacagcgaa tgaaatgtct 1740
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aacgtagacg tcaatggaaa aagtcataat ctccgtcaaa aatccaaccg ctcttcaca 1920
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<210> 12

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 12

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Gly Gly Met Ala Thr Tyr Cys Cys Ala Thr Thr Tyr Ala Ala Cys Ala
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Ala Gly Gly Cys
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<210> 13

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 13

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Ala Ala Ala Gly Ala Gly Ala Gly Asn Ala Cys Asn Asn Ala Asn Asn
 1             5             10             15

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Ala Asn Gly Ala
      20

```

<210> 14

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 14

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Thr Thr Gly Gly Ala Thr Cys Cys Gly Gly Ile Ala Cys Ile Ala Cys
 1             5             10             15

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Ile Gly Gly Ile Tyr Thr Ile Cys Cys Ile Ala Ala Arg Gly Gly
 20 25 30

<210> 15
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 15
 Thr Thr Gly Gly Ala Thr Cys Cys Gly Thr Ile Gly Thr Ile Gly Cys
 1 5 10 15
 Ile Cys Ala Arg Cys Ala Arg Gly Thr Ile Gly Ala Tyr Gly Gly
 20 25 30

<210> 16
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 16
 Cys Cys Ile Cys Thr Tyr Thr Ala Asp Ala Cys Arg Thr Ala Asp Gly
 1 5 10 15
 Cys Ile Cys Cys Ala Gly Cys Thr Gly Thr Ala
 20 25

<210> 17
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 17
 tttttttttt tttta

15

<210> 18
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 18

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15

<210> 19

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 19

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15

<210> 20

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 20

Cys Cys Asn Gly Gly Asn Gly Gly Ser Ala Arg Gly Ala
1 5 10

<210> 21

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (3)

<223> Variable amino acid

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<221> MOD_RES

<222> (5)..(6)

<223> Variable amino acid

<220>

<221> MOD_RES

<222> (8)

<223> Variable amino acid

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 1 5

<210> 22
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (23)
 <223> Inosine

<400> 22
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26

<210> 23
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 23
 atggctttcc ttctaatacc catctc

26

<210> 24
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 24
 ggggtgtaatg gacgagcaag gacttg

26